

[Sequence Listing]

<110> NEC Corporation and Dr. Masahiko KURODA

<120> Novel Cancer Gene And Its Use

5 <130>

<160> 2

<210> 1

10 <211>

<212> PRT

<213> Human

<400> 1

15 Met Thr Ser Arg Phe Gly Lys Thr Tyr Ser Arg Lys Gly Gly Asn Gly

1 5 10 15

Ser Ser Lys Phe Asp Glu Val Phe Ser Asn Lys Arg Thr Thr Leu Ser

20 25 30

Thr Lys Trp Gly Glu Thr Thr Phe Met Ala Lys Leu Gly Gln Lys Arg

20 35 40 45

Pro Asn Phe Lys Pro Asp Ile Gln Glu Ile Pro Lys Lys Pro Lys Val

50 55 60

Glu Glu Glu Ser Thr Gly Asp Pro Phe Gly Phe Asp Ser Asp Asp Glu

65 70 75 80

25 Ser Leu Pro Val Ser Ser Lys Asn Leu Ala Gln Val Lys Cys Ser Ser

		85		90		95										
	Tyr	Ser	Glu	Ser	Ser	Glu	Ala	Ala	Gln	Leu	Glu	Glu	Val	Thr	Ser	Val
		100		105		110										
	Leu	Glu	Ala	Asn	Ser	Lys	Ile	Ser	His	Val	Val	Val	Glu	Asp	Thr	Val
5		115		120		125										
	Val	Ser	Asp	Lys	Cys	Phe	Pro	Leu	Glu	Asp	Thr	Leu	Leu	Gly	Lys	Glu
		130		135		140										
	Lys	Ser	Thr	Asn	Arg	Ile	Val	Glu	Asp	Asp	Ala	Ser	Ile	Ser	Ser	Cys
	145		150		155		160									
10	Asn	Lys	Leu	Ile	Thr	Ser	Asp	Lys	Val	Glu	Asn	Phe	His	Glu	Glu	His
		165		170		175										
	Glu	Lys	Asn	Ser	His	His	Ile	His	Lys	Asn	Ala	Asp	Asp	Ser	Thr	Lys
		180		185		190										
	Lys	Pro	Asn	Ala	Glu	Thr	Thr	Val	Ala	Ser	Glu	Ile	Lys	Glu	Thr	Asn
15		195		200		205										
	Asp	Thr	Trp	Asn	Ser	Gln	Phe	Gly	Lys	Arg	Pro	Glu	Ser	Pro	Ser	Glu
	210		215		220											
	Ile	Ser	Pro	Ile	Lys	Gly	Ser	Val	Arg	Thr	Gly	Leu	Phe	Glu	Trp	Asp
	225		230		235		240									
20	Asn	Asp	Phe	Glu	Asp	Ile	Arg	Ser	Glu	Asp	Cys	Ile	Leu	Ser	Leu	Asp
		245		250		255										
	Ser	Asp	Pro	Leu	Leu	Glu	Met	Lys	Asp	Asp	Asp	Phe	Lys	Asn	Arg	Leu
		260		265		270										
	Glu	Asn	Leu	Asn	Glu	Ala	Ile	Glu	Glu	Asp	Ile	Val	Gln	Ser	Val	Leu
25		275		280		285										

	Arg	Pro	Thr	Asn	Cys	Arg	Thr	Tyr	Cys	Arg	Ala	Asn	Lys	Thr	Lys	Ser
	290			295			300									
	Ser	Gln	Gly	Ala	Ser	Asn	Phe	Asp	Lys	Leu	Met	Asp	Gly	Thr	Ser	Gln
	305			310			315			320						
5	Ala	Leu	Ala	Lys	Ala	Asn	Ser	Glu	Ser	Ser	Lys	Asp	Gly	Leu	Asn	Gln
	325			330			335									
	Ala	Lys	Lys	Gly	Gly	Val	Ser	Cys	Gly	Thr	Ser	Phe	Arg	Gly	Thr	Val
	340			345			350									
	Gly	Arg	Thr	Arg	Asp	Tyr	Thr	Val	Leu	His	Pro	Ser	Cys	Leu	Ser	Val
10	355			360			365									
	Cys	Asn	Val	Thr	Ile	Gln	Asp	Thr	Met	Glu	Arg	Ser	Met	Asp	Glu	Phe
	370			375			380									
	Thr	Ala	Ser	Thr	Pro	Ala	Asp	Leu	Gly	Glu	Ala	Gly	Arg	Leu	Arg	Lys
	385			390			395			400						
15	Lys	Ala	Asp	Ile	Ala	Thr	Ser	Lys	Thr	Thr	Thr	Arg	Phe	Arg	Pro	Ser
	405			410			415									
	Asn	Thr	Lys	Ser	Lys	Lys	Asp	Val	Lys	Leu	Glu	Phe	Phe	Gly	Phe	Glu
	420			425			430									
	Asp	His	Glu	Thr	Gly	Gly	Asp	Glu	Gly	Gly	Ser	Gly	Ser	Ser	Asn	Tyr
20	435			440			445									
	Lys	Ile	Lys	Tyr	Phe	Gly	Phe	Asp	Asp	Leu	Ser	Glu	Ser	Glu	Asp	Asp
	450			455			460									
	Glu	Asp	Asp	Asp	Cys	Gln	Val	Glu	Arg	Lys	Thr	Ser	Lys	Lys	Arg	Thr
	465			470			475			480						
25	Lys	Thr	Ala	Pro	Ser	Pro	Ser	Leu	Gln	Pro	Pro	Pro	Glu	Ser	Asn	Asp

	485	490	495
	Asn Ser Gln Asp Ser Gln Ser Gly Thr Asn Asn Ala Glu Asn Leu Asp		
	500	505	510
	Phe Thr Glu Asp Leu Pro Gly Val Pro Glu Ser Val Lys Lys Pro Ile		
5	515	520	525
	Asn Lys Gln Gly Asp Lys Ser Lys Glu Asn Thr Arg Lys Ile Phe Ser		
	530	535	540
	Gly Pro Lys Arg Ser Pro Thr Lys Ala Val Tyr Asn Ala Arg His Trp		
	545	550	555
10	Asn His Pro Asp Ser Glu Glu Leu Pro Gly Pro Pro Val Val Lys Pro		
	565	570	575
	Gln Ser Val Thr Val Arg Leu Ser Ser Lys Glu Pro Asn Gln Lys Asp		
	580	585	590
	Asp Gly Val Phe Lys Ala Pro Ala Pro Pro Ser Lys Val Ile Lys Thr		
15	595	600	605
	Val Thr Ile Pro Thr Gln Pro Tyr Gln Asp Ile Val Thr Ala Leu Lys		
	610	615	620
	Cys Arg Arg Glu Asp Lys Glu Leu Tyr Thr Val Val Gln His Val Lys		
	625	630	635
20	His Phe Asn Asp Val Val Glu Phe Gly Glu Asn Gln Glu Phe Thr Asp		
	645	650	655
	Asp Ile Glu Tyr Leu Leu Ser Gly Leu Lys Ser Thr Gln Pro Leu Asn		
	660	665	670
	Thr Arg Cys Leu Ser Val Ile Ser Leu Ala Thr Lys Cys Ala Met Pro		
25	675	680	685

Ser Phe Arg Met His Leu Arg Ala His Gly Met Val Ala Met Val Phe  
 690 695 700  
 Lys Thr Leu Asp Asp Ser Gln His His Gln Asn Leu Ser Leu Cys Thr  
 705 710 715 720  
 5 Ala Ala Leu Met Tyr Ile Leu Ser Arg Asp Arg Leu Asn Met Asp Leu  
 725 730 735  
 Asp Arg Ala Ser Leu Asp Leu Met Ile Arg Leu Leu Glu Leu Glu Gln  
 740 745 750  
 Asp Ala Ser Ser Ala Lys Leu Leu Asn Glu Lys Asp Met Asn Lys Ile  
 10 755 760 765  
 Lys Glu Lys Ile Arg Arg Leu Cys Glu Thr Val His Asn Lys His Leu  
 770 775 780  
 Asp Leu Glu Asn Ile Thr Thr Gly His Leu Ala Met Glu Thr Leu Leu  
 785 790 795 800  
 15 Ser Leu Thr Ser Lys Arg Ala Gly Asp Trp Phe Lys Glu Glu Leu Arg  
 805 810 815  
 Leu Leu Gly Gly Leu Asp His Ile Val Asp Lys Val Lys Glu Cys Val  
 820 825 830  
 Asp His Leu Ser Arg Asp Glu Asp Glu Glu Lys Leu Val Ala Ser Leu  
 20 835 840 845  
 Trp Gly Ala Glu Arg Cys Leu Arg Val Leu Glu Ser Val Thr Val His  
 850 855 860  
 Asn Pro Glu Asn Gln Ser Tyr Leu Ile Ala Tyr Lys Asp Ser Gln Leu  
 865 870 875 880  
 25 Ile Val Ser Ser Ala Lys Ala Leu Gln His Cys Glu Glu Leu Ile Gln

	885	890	895
	Gln Tyr Asn Arg Ala Glu Asp Ser Ile Cys Leu Ala Asp Ser Lys Pro		
	900	905	910
	Leu Pro His Gln Asn Val Thr Asn His Val Gly Lys Ala Val Glu Asp		
5	915	920	925
	Cys Met Arg Ala Ile Ile Gly Val Leu Leu Asn Leu Thr Asn Asp Asn		
	930	935	940
	Glu Trp Gly Ser Thr Lys Thr Gly Glu Gln Asp Gly Leu Ile Gly Thr		
	945	950	955
10	Ala Leu Asn Cys Val Leu Gln Val Pro Lys Tyr Leu Pro Gln Glu Gln		
	965	970	975
	Arg Phe Asp Ile Arg Val Leu Gly Leu Gly Leu Leu Ile Asn Leu Val		
	980	985	990
	Glu Tyr Ser Ala Arg Asn Arg His Cys Leu Val Asn Met Glu Thr Ser		
15	995	1000	1005
	Cys Ser Phe Asp Ser Ser Ile Cys Ser Gly Glu Gly Asp Asp Ser Leu		
	1010	1015	1020
	Arg Ile Gly Gly Gln Val His Ala Val Gln Ala Leu Val Gln Leu Phe		
	1025	1030	1035
20	Leu Glu Arg Glu Arg Ala Ala Gln Leu Ala Glu Ser Lys Thr Asp Glu		
	1045	1050	1055
	Leu Ile Lys Asp Ala Pro Thr Thr Gln His Asp Lys Ser Gly Glu Trp		
	1060	1065	1070
	Gln Glu Thr Ser Gly Glu Ile Gln Trp Val Ser Thr Glu Lys Thr Asp		
25	1075	1080	1085

Gly Thr Glu Glu Lys His Lys Lys Glu Glu Glu Asp Glu Glu Leu Asp

1090

1095

1100

Leu Asn Lys Ala Leu Gln His Ala Gly Lys His Met Glu Asp Cys Ile

1105

1110

1115

1120

5 Val Ala Ser Tyr Thr Ala Leu Leu Leu Gly Cys Leu Cys Gln Glu Ser

1125

1130

1135

Pro Ile Asn Val Thr Thr Val Arg Glu Tyr Leu Pro Glu Gly Asp Phe

1140

1145

1150

Ser Ile Met Thr Glu Met Leu Lys Lys Phe Leu Ser Phe Met Asn Leu

10

1155

1160

1165

Thr Cys Ala Val Gly Thr Thr Gly Gln Lys Ser Ile Ser Arg Val Ile

1170

1175

1180

Glu Tyr Leu Glu His Cys

1185

1190

15

<210> 2

<211> 3570

<212> DNA

<213> Human

20

<400> 2

atgacatcca gatttgggaa aacatacagt aggaaaggtg gaaatggcag ttcaaaattc 60

gatgaagtct ttccaacaa acggactacc cttagcacia aatggggaga gaccacattt 120

atggctaaat tagggcagaa gagggccaat ttcaaaccag atatccaaga aattccgaag 180

25 aaacctaaag tggaagaaga aagtactgga gatccttttg gatttgatag tgatgatgag 240

tctctaccag tttcttcaaa gaatttagcc caggttaagt gttcctctta ttcagaatct 300  
 agtgaagctg ctcaagttgga agaggtcact tcagtacttg aagctaatag caaaattagt 360  
 catgtggtcg ttgaagacac tgtcgtttct gataaatgct tccctttgga ggacacttta 420  
 cttgggaaag aaaagagcac aaaccgaatt gtagaagatg atgcaagcat aagtagctgt 480  
 5 aataaattaa taacttcaga taaagtggag aattttcatg aagaacatga aaagaatagt 540  
 caccatattc acaaaaatgc tgatgacagt actaagaaac ccaatgcaga aactacagtg 600  
 gcttctgaaa tcaaggaaac aaatgatact tggaactccc agtttgggaa aaggccagaa 660  
 tcaccatcag aaatatctcc aatcaaggga tctgttagaa ctggtttggt tgaatgggat 720  
 aatgattttg aagatatcag atcagaagac tgtattttta gtttggatag tgatcccctt 780  
 10 ttggagatga aggatgacga ttttaaaaat cgattggaaa atctgaatga agccattgag 840  
 gaagatattg tacaaagtgt tcttaggcca accaactgta ggacgtactg tagggccaat 900  
 aaaacgaaat cctcccaagg agcatcaaat tttgataagc tgatggacgg caccagtcag 960  
 gccttagcca aagcaaacag tgaatcgagt aaagatggcc tgaatcaggc aaagaaaggg 1020  
 ggtgtaagtt gtgggaccag ttttagaggg acagttggac ggactagaga ttacactggt 1080  
 15 ttacatccat cttgcttgct agtttgtaat gttaccatac aggatactat ggaacgcagc 1140  
 atggatgagt tcaactgcac cactcctgca gatttgggag aagctggtcg tctcagaaaa 1200  
 aaggcagata ttgcaacttc taagactact actagatttc gacctagtaa tactaaatcc 1260  
 aaaaaggatg ttaaaactga attttttgggt tttgaagatc atgagacagg aggtgatgaa 1320  
 ggaggttctg gaagttctaa ttacaaaatt aagtattttg gotttgatga tctcagttaa 1380  
 20 agcgaagatg atgaagatga tgactgtcaa gtagaaagaa agacaagcaa aaaaagaact 1440  
 aaaacagctc catcaccctc cttgcagcct cccccagaaa gcaatgataa ttcccaggac 1500  
 agtcagtctg gtactaaciaa tgcagaaaac ttggatttta cagaggactt gcctggtgtg 1560  
 cctgaaagtg tgaagaagcc cataaataaa caaggagata aatcaaagga aaataccaga 1620  
 aagattttta gtggcccaaa acggtcacc ccaaaaagctg tatataatgc cagacattgg 1680  
 25 aatcatccag attcagaaga actgcctggg ccaccagtag taaaacctca gagtgtcaca 1740



gtgaggctgt ottcaaagga accaaatcaa aaagatgatg gagtttttaa ggctcctgca 1800  
 ccaccatcca aagtgataaa aactgtgaca atacctactc agccctacca agatatagtt 1860  
 actgcactga aatgcagacg agaagacaaa gaattatata ctgtttgttca gcacgtgaag 1920  
 cacttcaacg atgtttgtaga atttgggtgaa aatcaagagt tcactgatga cattgagtac 1980  
 5 ttgttaagtg gottaaagag cactcagcct ctaaacacac gttgccttag tgttattagc 2040  
 ttggctacta aatgtgccat gccagtttt cgaatgcacc tgagagcaca tgggatggta 2100  
 gcaatgggtct ttaaaacctt ggatgattcc cagcaccatc agaattctgtc cctctgtaca 2160  
 gctgcctca tgtatatact gagtagagat cgtttgaaca tggatcttga tagagctagc 2220  
 ttagatctaa tgattcgact tttggaactg gaacaagatg cticacacgc caagctactg 2280  
 10 aatgaaaaag acatgaacaa aattaaagaa aaaatccgaa ggctctgtga aactgtacac 2340  
 aacaagcatc ttgatctaga aaatataacg actgggcatt tagctatgga gacattatta 2400  
 tcccttactt ctaaacgagc aggagactgg tttaaagaag aactccggct tttgggtggt 2460  
 ctggatcata ttgtagataa agtaaaagaa tgtgtggatc atttaagtag agatgaggat 2520  
 gaagagaaac tggtagcctc actatgggga gcagagagat gtttacgagt tttagaaagt 2580  
 15 gtaactgtgc ataatccga aaatcaaagc tacttgatag catataaaga ttcccaactt 2640  
 attgtttcat cagctaaagc attacagcat tgtgaagaac tgattcagca gtacaaccgt 2700  
 gctgaggaca gcatatgctt agctgacagt aagcctctgc ctcaccagaa tgtaactaac 2760  
 catgtaggca aagcagtgga ggactgcatg agggccatca tcgggggtgtt gcttaattta 2820  
 actaatgata atgagtgggg cagcaccaaa acaggagagc aggacggtct cataggcaca 2880  
 20 gogctgaact gtgtgcttca ggttccaaag tacctacctc aggagcagag atttgatatt 2940  
 cgagtgtctg gottaggtct gctgataaat ctagtggagt atagtgtcg gaatcggcac 3000  
 tgtcttgtca acatggaaac atcgtgctct tttgattctt ccatctgtag tggagaaggg 3060  
 gatgatagtt taaggatagg tggacaagtt catgctgtcc aggctttagt gcagctattc 3120  
 cttgagcgag agcgggcagc ccagctagca gaaagtaaaa cagatgagtt gatcaaagat 3180  
 25 gctcccacca ctcagcatga taagagtgga gagtggcaag aaacaagtgg agaaatacag 3240

tgggtgtcaa ctgaaaagac tgatggtaca gaagagaaac ataagaagga ggaggaggat 3300  
gaagaacttg acctcaataa agcccttcag catgccggca aacacatgga ggattgcatt 3360  
gtggcctcct acacggcact acttcttggg tgtctctgcc aggaaagtcc aatcaatgta 3420  
accactgtgc gggaatatct gccagaagga gacttttcaa taatgacaga gatgctcaaa 3480  
5 aaatttttga gttttatgaa tctcacttgt gctgttgga caactggcca gaaatctatc 3540  
tctagagtga ttgaatattt ggaacattgc 3570